



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12N 15/12, C07K 14/47, 16/18, G01N 33/566, C12Q 1/68, C12N 15/11, 15/62, A01K 67/027, A61K 38/00		A2	(11) International Publication Number: WO 00/58473
			(43) International Publication Date: 5 October 2000 (05.10.00)
(21) International Application Number: PCT/US00/08621 (22) International Filing Date: 31 March 2000 (31.03.00) (30) Priority Data: 60/127,607 31 March 1999 (31.03.99) US 60/127,636 2 April 1999 (02.04.99) US 60/127,728 5 April 1999 (05.04.99) US 09/540,763 30 March 2000 (30.03.00) US (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Applications US 60/127,607 (CIP) Filed on 31 March 1999 (31.03.99) US 60/127,636 (CIP) Filed on 2 April 1999 (02.04.99) US 60/127,728 (CIP) Filed on 5 April 1999 (05.04.99) US 09/540,763 (CIP) Filed on 30 March 2000 (30.03.00) (71) Applicant (for all designated States except US): CURAGEN CORPORATION [US/US]; 555 Long Wharf Drive, 11th Floor, New Haven, CT 06511 (US).		(72) Inventors; and (75) Inventors/Applicants (for US only): SHIMKETS, Richard, A. [US/US]; 191 Leete Street, West Haven, CT 06516 (US). LEACH, Martin [GB/US]; 884 School Street, Webster, MA 01570 (US). (74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky and Popeo, P.C., One Financial Center, Boston, MA 02111 (US). (81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).	
		Published <i>Without international search report and to be republished upon receipt of that report.</i>	
(54) Title: NUCLEIC ACIDS INCLUDING OPEN READING FRAMES ENCODING POLYPEPTIDES; "ORFX"			
(57) Abstract			
<p>The present invention provides open reading frames ORFX, encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.</p>			

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

2180	87630197 (4379, 4380)	Novel Protein sim. GBank gij132575sp P28315 RIN1_RAT - RIBONUCLEASE INHIBITOR		nucleaseinhib	22278998, 22278999, 29331822, 29331824, 29331826, 265008, 264610, 60170831, 55812038, 52644296, 265010, 265018, 264685, 264688, 56181562, 21908789, 35685917, 265022, 60170394, 22279000
2181	96188628 (4381, 4382)	Novel Protein sim. GBank gij5327002 emb CAB46272.1 - (Y18503) XAP-5-like protein [Homo sapiens]			29331825, 29331828, 29331830, 284510, 264511, 264910, 264593, 264594, 264556, 284559
2182	11126316 (4383, 4384)	Novel Protein sim. GBank gij462800 sp P34400 MI10 CAEL - MIG-10 PROTEIN	Contains protein domain (PF00169) - PH domain		284558
2183	94140073 (4385, 4386)	Novel Protein sim. GBank gij5420389 emb CAB46680.1 - (AJ243480) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	56181888, 29331825, 29331827, 264508, 264809, 265008, 264592, 60432228, 284288, 264684, 264768, 35695917, 33657023, 60431802, 60431828, 55810764, 55811576, 65274791, 35695955, 60431850, 56182323, 60432113
2184	21416714 (4387, 4388)	Novel Protein sim. GBank gij2773341 (AF040854) - putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]			284592
2185	88083023 (4389, 4390)	Novel Protein sim. GBank gij2832783 emb CAA15685.1 - (AL009191) /prediction=(method:: prediction=(method:: /match=(desc:: /match=(desc:: /motif=(desc:: [Drosophila melanogaster]		UNCLASSIFIED	22278998, 22278999, 35686052, 265006, 21908754, 265017, 35695917, 285021, 265022, 35695955
2186	88081631 (4391, 4392)	Novel Protein sim. GBank gij5262487 emb CAB45699.1 - (AL080076) hypothetical protein [Homo sapiens]		collagen	56182575, 35696286, 22278997, 22278999, 264259, 29331822, 66714117, 60432288, 29331827, 35696052, 29331828, 264508, 52644045, 56182435, 284510, 265007, 265008, 265009, 60433438, 55812038, 285010, 285011, 264448, 264288, 264686, 264687, 52644229, 21906765, 21908786, 21908787, 35695917, 265022, 264691, 33657023, 264693, 18108370, 18108376, 35696423, 55811578, 65274791, 35693855, 264636, 56182323, 18108385
2187	85073813 (4393, 4394)	Novel Protein sim. GBank gij4628567 gb AAD3404.1 AF151807 - (AF151807) CGI-49 protein [Homo sapiens]			264768, 264769, 21906765, 21908766, 21908767, 28148627, 55811857, 35696286, 265020, 22278998, 265021, 264259, 33657023, 264683, 29331824, 35696052, 29331828, 18108370, 35695955, 264113, 265008, 264910, 60432229, 56182323, 33657402, 264758, 63373044, 21908754, 265018, 265019, 22278002, 264482, 264448, 264585, 264288, 264369
2188	88060914 (4395, 4396)	Novel Protein sim. GBank gij3548787 (AC005622) - R30953.1 [Homo sapiens]		UNCLASSIFIED	

This Page Blank (uspto)

1015	95418879 (2029, 2030)	Novel Protein sim. GBank gi 159895 (AF063095) - SELL [Mus musculus]	Contains protein domain (PF00040) - struct Fibronectin type II domain		22278994, 22278995, 56984075, 22278996, 22278999, 264259, 29331825, 29331828, 264807, 56182435, 264510, 264591, 264593, 60433356, 264594, 55812038, 264758, 21908754, 33657084, 265010, 264600, 265017, 265018, 265019, 18108351, 21908765, 21908768, 21908767, 21908768, 55811957, 265022, 33657023, 65274820, 33657182, 32833988, 18108370, 18108377, 55811576, 35896423, 264630, 22279000, 264565
1016	79559694 (2031, 2032)	Novel Protein sim. GBank gi 25069694 P41407 ACPD_ECOLI - ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)	esterase		264686, 264693
1017	11069213 (2033, 2034)	Novel Protein sim. GBank gi 5103943 b BAA79259.1 - (AP000059) 802aa long hypothetical oligopeptide-binding protein oppA [Aeropyrum pernix]	transport	Contains protein domain (PF00498) - Bacterial extracellular solute-binding proteins, family 5	264600
1018	80072430 (2035, 2036)	Novel Protein sim. GBank gi 4483973 emb CA839032.1 - (AL034559) predicted using hexExon; MAL397.14 (PFC0825a), Hypothetical protein, len: 488 aa [Plasmodium falciparum]			22278996, 26148627, 264563
1019	11703807 (2037, 2038)		UNCLASSIFIED		264686
1020	80234432 (2039, 2040)				264508, 264509, 264512, 264600, 264762, 264768, 264689, 18108370, 264636, 264638, 264488
1021	37036243 (2041, 2042)	Novel Protein sim. GBank gi 4633607 gb AAD26859.1 AF12779 - (AF127795) trehalose biosynthetic enzyme TreY [Rhizobium leguminosarum bv. viciae]	synthase		264768
1022	80502627 (2043, 2044)	Novel Protein sim. GBank gi 1781230 emb CA806277 - (283857) hypothetical protein Rv3137 [Mycobacterium tuberculosis]	phosphatase	Contains protein domain (PF00459) - inositol monophosphatase family	35695032, 264508, 265008, 265009, 264769, 18108387, 264563
1023	11389341 (2045, 2046)	Novel Protein sim. GBank gi 3777495 (U92083) - calcium transporting ATPase [Pichia angustia]	ATPase-associated	Contains protein domain (PF00122) - E1-E2 ATPase	264593
1024	80057128 (2047, 2048)		UNCLASSIFIED		52648842, 33657402, 33657023, 18108379, 55811576, 264631, 264556, 264557, 264558, 18108388, 264566
1025	78844200 (2049, 2050)	Novel Protein sim. GBank gi 3463045 emb CAA20558 - (AL031371) putative transport system permease protein [Streptomyces coelicolor]	transport		264693
1026	80025946 (2051, 2052)	Novel Protein sim. GBank gi 174922 sp Q02322 UVRD_HAEIN - DNA HELICASE II [Novel Protein sim. GBank gi 4757728 ref NP_004886.1 pAGTA - angiotensin/vasopressin receptor AII/AVP-like	helicase		264602
1027	17659234 (2053, 2054)	Novel Protein sim. GBank	UNCLASSIFIED		265017

This Page Blank (uspto)

8. The vector of claim 7, wherein said vector is an expression vector.
9. A host cell comprising the isolated nucleic acid molecule of claim 1.
10. A substantially purified polypeptide comprising an amino acid sequence at least 80% identical to a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO: 2*n*, wherein *n* is any integer 1-3161.
11. The polypeptide of claim 10, wherein said polypeptide comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 2*n*, wherein *n* is any integer 1-3161.
12. An antibody that selectively binds to the polypeptide of claim 10.
13. A pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a therapeutic selected from the group consisting of:
 - a) the nucleic acid of claim 1;
 - b) the polypeptide of claim 10; and
 - c) the antibody of claim 12;and a pharmaceutically acceptable carrier.
14. A kit comprising in one or more containers, a therapeutically or prophylactically effective amount of the pharmaceutical composition of claim 13.
15. A method of producing the polypeptide of claim 10, said method comprising culturing the host cell of claim 9 under conditions in which the nucleic acid molecule is expressed.
16. A method of detecting the presence of the polypeptide of claim 10 in a sample, comprising contacting the sample with a compound that selectively binds to said polypeptide under conditions allowing the formation of a complex between said polypeptide and said

What is claimed is:

1. An isolated nucleic acid molecule encoding a polypeptide comprising an amino acid sequence that is at least 85% identical to a polypeptide including an amino acid sequence selected from the group consisting of SEQ ID NO:2 n , wherein n is any integer 1-3161, or the complement thereof.
2. The isolated nucleic acid molecule of claim 1, said molecule hybridizing under stringent conditions to a nucleic acid sequence complementary to a nucleic acid molecule comprising the sequence of nucleotides selected from the group consisting of SEQ ID NO:2 n , wherein n is any integer 1-3161, or the complement thereof.
3. The isolated nucleic acid molecule of claim 1, said molecule encoding a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO: 2 n , wherein n is any integer 1-3161, or an amino acid sequence comprising one or more conservative substitutions in the amino acid sequence selected from the group consisting of SEQ ID NO: 2 n .
4. The isolated nucleic acid molecule of claim 1, wherein said molecule encodes a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO: 2 n , wherein n is any integer 1-3161.
5. The isolated nucleic acid molecule of claim 1, wherein said molecule comprises the sequence of nucleotides selected from the group consisting of SEQ ID NO:2 n -1, wherein n is any integer 1-3161, or the complement thereof.
6. An oligonucleotide less than 100 nucleotides in length and comprising at least 10 contiguous nucleotides selected from the group consisting of SEQ ID NO:2 n -1, wherein n is any integer 1-3161, or the complement thereof.
7. A vector comprising the nucleic acid molecule of claim 1.

compound, and detecting said complex, if present, thereby identifying said polypeptide in said sample.

17. A method of detecting the presence of a nucleic acid molecule of claim 1 in a sample, the method comprising contacting the sample with a nucleic acid probe or primer that selectively binds to the nucleic acid molecule and determining whether the nucleic acid probe or primer bound to the nucleic acid molecule of claim 1 is present in the sample.

18. A method for modulating the activity of the polypeptide of claim 10, the method comprising contacting a cell sample comprising the polypeptide of claim 10 with a compound that binds to said polypeptide in an amount sufficient to modulate the activity of the polypeptide.

19. The use of a therapeutic in the manufacture of a medicament for treating a syndrome associated with a ORFX-associated disorder, wherein said therapeutic is selected from the group consisting of:

- a) the nucleic acid of claim 1;
- b) the polypeptide of claim 10; and
- c) the antibody of claim 12.

20. A method for screening for a modulator of activity or of latency or predisposition to an ORFX-associated disorder, said method comprising:

- a) contacting a test compound with the polypeptide of claim 10; and
- b) determining if said test compound binds to said polypeptide,

wherein binding of said test compound to said polypeptide indicates the test compound is a modulator of activity or of latency or predisposition to an ORFX-associated disorder.

21. A method for screening for a modulator of activity or of latency or predisposition to an ORFX-associated disorder, said method comprising:

- a) administering a test compound to a test subject at an increased risk ORFX-associated disorder, wherein said test subject recombinantly expresses a polypeptide encoded by the nucleotide of claim 1;

- b) measuring expression the activity of said protein in said test subject;
- c) measuring the activity of said protein in a control subject that recombinantly expresses said protein and is not at increased risk for an ORFX-associated disorder; and
- d) comparing expression of said protein in said test subject and said control subject, wherein a change in the activity of said protein in said test subject relative to said control subject indicates the test compound is a modulator or of latency of predisposition to an ORFX-associated disorder.

22. The method of claim 20, wherein said test animal is a recombinant test animal that expresses a test protein transgene or expresses said transgene under the control of a promoter at an increased level relative to a wild-type test animal, and wherein said promoter is not the native gene promoter of said transgene.

23. A method for determining the presence of or predisposition to a disease associated with altered levels of a polypeptide of claim 11 in a subject, the method comprising:

- a) measuring the amount of the polypeptide in a sample from said subject; and
- b) comparing the amount of said polypeptide in step (a) to the amount of the polypeptide present in a control sample,

wherein an alteration in the level of the polypeptide in step (a) as compared to the control sample indicates the presence of or predisposition to a disease in said subject.

24. The method of claim 23, wherein said subject is a human.

25. A method for determining the presence of or predisposition to a disease associated with altered levels the nucleic acid molecule of claim 1 in a subject, the method comprising:

- a) measuring the amount of the nucleic acid in a sample from the mammalian subject; and
- b) comparing the amount of said nucleic acid in step (a) to the amount of the nucleic acid present in a control sample,

wherein an alteration in the level of the nucleic acid in step (a) as compared to the control sample indicates the presence of or predisposition to said disease in said subject.

26. The method of claim 25, wherein said subject is a human.

27. A method of treating or preventing a pathological condition associated with an ORFX-associated disorder in a subject, the method comprising administering to said subject polypeptide of claim 10 in an amount sufficient to alleviate or prevent said pathological condition.

28. The method of claim 27, wherein said subject is a human.

29. A method of treating or preventing a pathological condition associated with an ORFX-associated disorder in a subject, the method comprising administering to said subject nucleic acid molecule of claim 1 in an amount sufficient to alleviate or prevent said pathological condition.

30. The method of claim 29, wherein said subject is a human.

31. A method of treating or preventing a pathological condition associated with an ORFX-associated disorder in a subject, the method comprising administering to said subject antibody of claim 12 in an amount sufficient to alleviate or prevent said pathological condition.

32. The method of claim 31, wherein said subject is a human.

<212> DNA
<213> Homo sapiens

<400> 2051
gagcaaaact atcgttctac cggcaatatt ctgaaaagtg ccaaccaact tatttcgaat
60
aatagtgatc gtctcggtaa gaatttatgg accgacggtg aaatggggga gccagtaggt
120
atttatgcag catttaatga attagatgag gcaaaatttg tggcgtctca aatccaaaat
180
tgggtagatg atgggtggga attagatgat tgtgctgttt tatatcgtag taatagccaa
240
tctcgtgtta ttgaagaagc cttgattcgt tgccaaattc cttatcgaat ttatggcggg
300
atgcgattct tcgaacgcca agaaattaaa gatgcgttgg catatttacg ttttaattaat
360
aatcgtcaag atgatgccgc atttgagcgt gtgattaata cgcctacgcg t
411

<210> 2052
<211> 137
<212> PRT
<213> Homo sapiens

<400> 2052
Glu Gln Asn Tyr Arg Ser Thr Gly Asn Ile Leu Lys Ser Ala Asn Gln
1 5 10 15
Leu Ile Ser Asn Asn Ser Asp Arg Leu Gly Lys Asn Leu Trp Thr Asp
20 25 30
Gly Glu Met Gly Glu Pro Val Gly Ile Tyr Ala Ala Phe Asn Glu Leu
35 40 45
Asp Glu Ala Lys Phe Val Ala Ser Gln Ile Gln Asn Trp Val Asp Asp
50 55 60
Gly Gly Glu Leu Asp Asp Cys Ala Val Leu Tyr Arg Ser Asn Ser Gln
65 70 75 80
Ser Arg Val Ile Glu Ala Leu Ile Arg Cys Gln Ile Pro Tyr Arg
85 90 95
Ile Tyr Gly Gly Met Arg Phe Phe Glu Arg Gln Glu Ile Lys Asp Ala
100 105 110
Leu Ala Tyr Leu Arg Leu Ile Asn Asn Arg Gln Asp Asp Ala Ala Phe
115 120 125
Glu Arg Val Ile Asn Thr Pro Thr Arg
130 135

<210> 2053
<211> 287
<212> DNA
<213> Homo sapiens

<400> 2053
nccatggaag ccttcaatct tgtaagagaa agtgaacagc tgttttccat atgccaaatc
60
ccgctcctct gctggatcct gtgtaccagt ctgaagcaag agatgcagaa aggaaaagac
120

This Page Blank (uspto)

ctggccctga cctgccagag cactacctct gtgtactcct ctttcgtctt taacctgttc
 180
 acacctgagg gtgccgagg cccgactccg caaaccagc accagctgaa ggccctgtgc
 240
 tccctggctg cagagggtat gtggacagac acatttgagt tttgtga
 287

<210> 2054
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 2054
 Ile Cys Gln Ile Pro Leu Leu Cys Trp Ile Leu Cys Thr Ser Leu Lys
 1 5 10 15
 Gln Glu Met Gln Lys Gly Lys Asp Leu Ala Leu Thr Cys Gln Ser Thr
 20 25 30
 Thr Ser Val Tyr Ser Ser Phe Val Phe Asn Leu Phe Thr Pro Glu Gly
 35 40 45
 Ala Glu Gly Pro Thr Pro Gln Thr Gln His Gln Leu Lys Ala Leu Cys
 50 55 60
 Ser Leu Ala Ala Glu Gly Met Trp Thr Asp Thr Phe Glu Phe Cys
 65 70 75

<210> 2055
 <211> 298
 <212> DNA
 <213> Homo sapiens

<400> 2055
 nnacgcgttg ttatgaacaa tgacgggtgc ctctaccccg atacctgcgt ggggtactgat
 60
 tcccacacca ccatggaaaa tgggtcttggc attctgggct ggggcgtcgg tgggtattgaa
 120
 gccgaggctg ctatgcttgg ccagcccatc tccatgctta tccccgtgt tgggtggcttt
 180
 aaacttactg gccaaacaca gccgggtgac accgctacag atgttggtct taccattact
 240
 gatatgcttc gccagcatgg tgtgggtgga aaattcgggg aattctatgg gggaagcg
 298

<210> 2056
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 2056
 Xaa Arg Val Val Met Asn Asn Asp Gly Val Leu Tyr Pro Asp Thr Cys
 1 5 10 15
 Val Gly Thr Asp Ser His Thr Thr Met Glu Asn Gly Leu Gly Ile Leu
 20 25 30
 Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Ala Met Leu Gly Gln
 35 40 45
 Pro Ile Ser Met Leu Ile Pro Arg Val Val Gly Phe Lys Leu Thr Gly

This Page Blank (uspto)

ctgctggcgg cgggagagge cggcaccttc gacgtggccg tgggtggatgc ggacaaggag
 480
 aactgctccg cctactacga gcgctgcctg cagctgctgc gacccggagg catcctcgcc
 540
 gtcctcagag tcctgtggcg cgggaaggtg ctgcaacctc cgaaagggga cgtggcggcc
 600
 gagtgtgtgc gaaacctaaa cgaacgcac cggcgggacg tcagggtcta catcagcctc
 660
 ctgccccctgg gcgatggact caccttggcc ttcaagatct agggctggcc cctagtgagt
 720
 gggctcgagg gaggggttggc tgggaacccc aggaattgac cctgagtttt aaattcgaaa
 780
 ataaagtggg gctggggacac acgaaaaaaaa aa
 812

<210> 4378
 <211> 233
 <212> PRT
 <213> Homo sapiens

<400> 4378
 Xaa Leu Gly Arg Arg Cys Pro Pro Trp Arg Gly Arg Arg Glu Gln Gly
 1 5 10 15
 Leu Leu Pro Pro Glu Asp Ser Arg Leu Trp Gln Tyr Leu Leu Ser Arg
 20 25 30
 Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu Thr Leu
 35 40 45
 Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln Ala Gln Leu
 50 55 60
 Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys Ala Leu Asp Leu
 65 70 75 80
 Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu Ala Leu Pro
 85 90 95
 Ala Asp Gly Arg Val Val Thr Cys Glu Val Asp Ala Gln Pro Pro Glu
 100 105 110
 Leu Gly Arg Pro Leu Trp Arg Gln Ala Glu Ala Glu His Lys Ile Arg
 115 120 125
 Leu Arg Leu Lys Pro Ala Leu Glu Thr Leu Asp Glu Leu Leu Ala Ala
 130 135 140
 Gly Glu Ala Gly Thr Phe Asp Val Ala Val Val Asp Ala Asp Lys Glu
 145 150 155 160
 Asn Cys Ser Ala Tyr Tyr Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly
 165 170 175
 Gly Ile Leu Ala Val Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln
 180 185 190
 Pro Pro Lys Gly Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu
 195 200 205
 Arg Ile Arg Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly
 210 215 220
 Asp Gly Leu Thr Leu Ala Phe Lys Ile
 225 230

<210> 4379
 <211> 2347

This Page Blank (uspto)

<212> DNA

<213> Homo sapiens

<400> 4379

ngaggaccaa gccatgcgtg cctttgagct aatgaggagc aacgcggccc tgttccagct
60
gggctcggcc ccgcgggtgtg ctggattgtg tgcacgactc tgaagctgca gatggagaag
120
ggggaggacc cggccccac ctgcctcacc cgcacggggc tgttctcgcg tttcctctgc
180
agccggttcc cgcggggcgc acagctgcgg ggcgcgctgc ggacgctgag cctcctggcc
240
gcgcagggcc tgtgggcgca gacgtccgtg cttcaccgag aggatctgga aaggctcggg
300
gtgcaggagt ccgacctcg tctgttcttg gacggagaca tcctccgcca ggacagagtc
360
tccaaaggct gctactcctt catccacctc agcttccagc agtttctcac tgccctgttc
420
tacaccctgg agaaggagga ggaagaggat agggacggcc acacctggga cattggggac
480
gtacagaagc tgctttccgg agtagaaaga ctcaggaacc ccgacctgat ccaagcaggc
540
tactactcct ttggcctcgc taacgagaag agagccaagg agttggaggc cacttttggc
600
tgccggatgt caccggacat caaacaggaa ttgctgcgat gcgacataag ttgtaagggt
660
ggacattcaa cggtgacaga cctgcaggag ctgctcggct gtctgtacga gtctcaggag
720
gaggagctgg tgaaggaggt gatggctcag ttcaaagaaa tatccctgca cttaaatgca
780
gtagacgttg tgccatcttc attctgcgtc aagcactgtc gaaacctgca gaaaatgtca
840
ctgcaggtaa taaaggagaa tctcccgag aatgtcactg cgtctgaatc agacgccgag
900
gttgagagat cccaggatga tcagcacatg cttcctttct ggacggacct ttgttcata
960
tttggatcaa ataaggatct gatgggtcta gcaatcaatg atagctttct cagtgcctcc
1020
ctagtaagga tcctgtgtga acaaatagcc tctgacacct gtcattctca gagagtgggtg
1080
ttcaaaaaca tttccccagc tgatgctcat cggaaacctn tgccctnnagc tcttcgaggt
1140
cacaagactg taacgtatct gacccttcaa ggcaatgacc aggatgatat gtttcccgca
1200
ttgtgtgagg tcttgagaca tccagaatgt aacctgcgat atctcgggtt ggtgtcttgt
1260
tccgctacca ctcagcagtg ggctgatctc tccttggccc ttgaagtcaa ccagtccttg
1320
acgtgcgtaa acctctccga caatgagctt ctggatgagg gtgctaagtt gctgtacaca
1380
actttgagac accccaagtg ctttctgcag aggttgtcgt tggaaaactg tcaccttaca
1440
gaagccaatt gcaaggacct tgctgctgtg ttggttgtca gccgggagct gacacacctg
1500

This Page Blank (uspto)

tgcttgccca agaaccccat tgggaatata ggggtgaagt ttctgtgtga gggcttgagg
 1560
 taccctgagt gtaaactgca gaccttggtg ctttggaact ggcacataac tagcgatggc
 1620
 tgctgcgata tcacaaagct tctccaagaa aaatcaagcc tgttgtgttt ggatctgggg
 1680
 ctgaatcaca taggagttaa ggggaatgaag ttctgtgtg aggctttgag gaaaccactg
 1740
 tgcaacttga gatgtctgtg gttgtgggga tgttccatcc ctccgttcag ttgtgaagac
 1800
 gtctgctctg ccctcagctg caaccagagc ctctgctactc tggacctggg tcagaatccc
 1860
 ttgggggtcta gtggagtga gatgctgttt gaaaccttga catgttccag tggcaccctc
 1920
 cggacactca ggttgaaaat agatgacttt aatgatgaac tcaataagct gctggaagaa
 1980
 atagaagaaa aaaacccaca actgattatt gatactgaga aacatcatcc ctgggaagaa
 2040
 aggccttctt ctcatgactt catgatctga atcccccgga gtcattcatt ctccatgaag
 2100
 tcatcgattt tccaggtgtg ggtgaactgc ctgtgactcc tctctctccc cgccccctacc
 2160
 cctcagggat aatgagttca ttgctgggct agatgtttta gccatgatcc tgccctctgtt
 2220
 ttatacctgc acacatcctt atctttgtta catatgaaat atctgtatca cgggttatatt
 2280
 gagagaaata aaggtgagag cattcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
 2340
 aaaaaaa
 2347

<210> 4380
 <211> 652
 <212> PRT
 <213> Homo sapiens

<400> 4380
 Met Glu Lys Gly Glu Asp Pro Val Pro Thr Cys Leu Thr Arg Thr Gly
 1 5 10 15
 Leu Phe Leu Arg Phe Leu Cys Ser Arg Phe Pro Arg Gly Ala Gln Leu
 20 25 30
 Arg Gly Ala Leu Arg Thr Leu Ser Leu Leu Ala Ala Gln Gly Leu Trp
 35 40 45
 Ala Gln Thr Ser Val Leu His Arg Glu Asp Leu Glu Arg Leu Gly Val
 50 55 60
 Gln Glu Ser Asp Leu Arg Leu Phe Leu Asp Gly Asp Ile Leu Arg Gln
 65 70 75 80
 Asp Arg Val Ser Lys Gly Cys Tyr Ser Phe Ile His Leu Ser Phe Gln
 85 90 95
 Gln Phe Leu Thr Ala Leu Phe Tyr Thr Leu Glu Lys Glu Glu Glu
 100 105 110
 Asp Arg Asp Gly His Thr Trp Asp Ile Gly Asp Val Gln Lys Leu Leu
 115 120 125
 Ser Gly Val Glu Arg Leu Arg Asn Pro Asp Leu Ile Gln Ala Gly Tyr

This Page Blank (uspto)

tgcttgcca agaaccccat tgggaataca ggggtgaagt ttctgtgtga gggcttgagg
 1560
 taccocgagt gtaaaactgca gaccttggtg ctttggaact ggcacataac tagcgatggc
 1620
 tgctgcgatc tcacaaagct tctccaagaa aaatcaagcc tgttgtgttt ggatctgggg
 1680
 ctgaatcaca taggagttaa ggggaatgaag ttctgtgtg aggctttgag gaaaccactg
 1740
 tgcaacttga gatgtctgtg gttgtgggga tgttccatcc ctccgttcag ttgtgaagac
 1800
 gtctgtctg ccctcagctg caaccagagc ctcgtcactc tggacctggg tcagaatccc
 1860
 ttgggggtcta gtggagtga gatgctgttt gaaaccttga catgttccag tggcacccctc
 1920
 cggacactca ggttgaaaat agatgacttt aatgatgaac tcaataagct gctggaagaa
 1980
 atagaagaaa aaaacccaca actgattatt gatactgaga aacatcatcc ctgggaagaa
 2040
 aggccctctt ctcatgactt catgatctga atccccccga gtcattcatt ctccatgaag
 2100
 tcatcgattt tccaggtgtg ggtgaactgc ctgtgactcc tctcctcccc cgcccctacc
 2160
 cctcagggat aatgagttca ttgctgggct agatgtttta gccatgatcc tgcctctgtt
 2220
 ttatacctgc acacatcctt atctttgtta catatgaaat atctgtatca cgggtatatt
 2280
 gagagaaata aaggtgagag cattcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
 2340
 aaaaaaa
 2347

<210> 4380

<211> 652

<212> PRT

<213> Homo sapiens

<400> 4380

Met	Glu	Lys	Gly	Glu	Asp	Pro	Val	Pro	Thr	Cys	Leu	Thr	Arg	Thr	Gly
1				5					10					15	
Leu	Phe	Leu	Arg	Phe	Leu	Cys	Ser	Arg	Phe	Pro	Arg	Gly	Ala	Gln	Leu
			20					25					30		
Arg	Gly	Ala	Leu	Arg	Thr	Leu	Ser	Leu	Leu	Ala	Ala	Gln	Gly	Leu	Trp
			35					40				45			
Ala	Gln	Thr	Ser	Val	Leu	His	Arg	Glu	Asp	Leu	Glu	Arg	Leu	Gly	Val
			50			55				60					
Gln	Glu	Ser	Asp	Leu	Arg	Leu	Phe	Leu	Asp	Gly	Asp	Ile	Leu	Arg	Gln
65					70					75				80	
Asp	Arg	Val	Ser	Lys	Gly	Cys	Tyr	Ser	Phe	Ile	His	Leu	Ser	Phe	Gln
				85					90					95	
Gln	Phe	Leu	Thr	Ala	Leu	Phe	Tyr	Thr	Leu	Glu	Lys	Glu	Glu	Glu	Glu
			100					105					110		
Asp	Arg	Asp	Gly	His	Thr	Trp	Asp	Ile	Gly	Asp	Val	Gln	Lys	Leu	Leu
			115				120					125			
Ser	Gly	Val	Glu	Arg	Leu	Arg	Asn	Pro	Asp	Leu	Ile	Gln	Ala	Gly	Tyr

This Page Blank (uspto)

	130					135					140						
Tyr	Ser	Phe	Gly	Leu	Ala	Asn	Glu	Lys	Arg	Ala	Lys	Glu	Leu	Glu	Ala		
145					150					155					160		
Thr	Phe	Gly	Cys	Arg	Met	Ser	Pro	Asp	Ile	Lys	Gln	Glu	Leu	Leu	Arg		
				165					170						175		
Cys	Asp	Ile	Ser	Cys	Lys	Gly	Gly	His	Ser	Thr	Val	Thr	Asp	Leu	Gln		
			180					185						190			
Glu	Leu	Leu	Gly	Cys	Leu	Tyr	Glu	Ser	Gln	Glu	Glu	Glu	Leu	Val	Lys		
		195					200					205					
Glu	Val	Met	Ala	Gln	Phe	Lys	Glu	Ile	Ser	Leu	His	Leu	Asn	Ala	Val		
	210					215					220						
Asp	Val	Val	Pro	Ser	Ser	Phe	Cys	Val	Lys	His	Cys	Arg	Asn	Leu	Gln		
225					230					235					240		
Lys	Met	Ser	Leu	Gln	Val	Ile	Lys	Glu	Asn	Leu	Pro	Glu	Asn	Val	Thr		
				245					250						255		
Ala	Ser	Glu	Ser	Asp	Ala	Glu	Val	Glu	Arg	Ser	Gln	Asp	Asp	Gln	His		
		260						265						270			
Met	Leu	Pro	Phe	Trp	Thr	Asp	Leu	Cys	Ser	Ile	Phe	Gly	Ser	Asn	Lys		
		275					280					285					
Asp	Leu	Met	Gly	Leu	Ala	Ile	Asn	Asp	Ser	Phe	Leu	Ser	Ala	Ser	Leu		
	290					295					300						
Val	Arg	Ile	Leu	Cys	Glu	Gln	Ile	Ala	Ser	Asp	Thr	Cys	His	Leu	Gln		
305					310					315					320		
Arg	Val	Val	Phe	Lys	Asn	Ile	Ser	Pro	Ala	Asp	Ala	His	Arg	Asn	Leu		
				325					330						335		
Xaa	Pro	Xaa	Ala	Leu	Arg	Gly	His	Lys	Thr	Val	Thr	Tyr	Leu	Thr	Leu		
		340						345					350				
Gln	Gly	Asn	Asp	Gln	Asp	Asp	Met	Phe	Pro	Ala	Leu	Cys	Glu	Val	Leu		
		355				360						365					
Arg	His	Pro	Glu	Cys	Asn	Leu	Arg	Tyr	Leu	Gly	Leu	Val	Ser	Cys	Ser		
	370					375					380						
Ala	Thr	Thr	Gln	Gln	Trp	Ala	Asp	Leu	Ser	Leu	Ala	Leu	Glu	Val	Asn		
385					390					395					400		
Gln	Ser	Leu	Thr	Cys	Val	Asn	Leu	Ser	Asp	Asn	Glu	Leu	Leu	Asp	Glu		
				405					410					415			
Gly	Ala	Lys	Leu	Leu	Tyr	Thr	Thr	Leu	Arg	His	Pro	Lys	Cys	Phe	Leu		
		420						425					430				
Gln	Arg	Leu	Ser	Leu	Glu	Asn	Cys	His	Leu	Thr	Glu	Ala	Asn	Cys	Lys		
		435					440					445					
Asp	Leu	Ala	Ala	Val	Leu	Val	Val	Ser	Arg	Glu	Leu	Thr	His	Leu	Cys		

This Page Blank (uspto)

```
<210> 4381
<211> 1638
<212> DNA
<213> Homo sapiens
```

3572

This Page Blank (uspto)

104